continuation, by the named inventors hereof and assigned to the same assignee and claims priority in said prior filed applications."

IN THE CLAIMS:

Please amend claim 1 as follows:

1. (Twice Amended) A method of staining targeted chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe [probes] of greater than about 50,000 bases, wherein said targeted chromosomal material is a genetic rearrangement associated with chromosome 3 and/or chromosome 17 in humans, said method comprising contacting said chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, allowing said probe to bind to said targeted chromosomal material and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

Please add new claims 48-50 as follows:

--48. A method of staining targeted chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein said targeted chromosomal material is a genetic rearrangement associated with chromosome 3 and/or chromosome 17 in humans, said method comprising contacting said chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 40 kb, allowing said probe to bind to